

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/698,070A  
Source: IFW16  
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IFW16

## RAW SEQUENCE LISTING

DATE: 01/31/2006

PATENT APPLICATION: US/10/698,070A

TIME: 11:02:30

Input Set : A:\221749.ST25.txt

Output Set: N:\CRF4\01312006\J698070A.raw

3 <110> APPLICANT: GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY  
 4 THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES  
 5 KAYE, FREDERIC J.  
 6 KOMIYA, TAKEFUMI  
 8 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A  
 CHIMERIC  
 9 GENE  
 11 <130> FILE REFERENCE: 221749  
 13 <140> CURRENT APPLICATION NUMBER: 10/698,070A  
 14 <141> CURRENT FILING DATE: 2003-10-30  
 16 <160> NUMBER OF SEQ ID NOS: 12  
 18 <170> SOFTWARE: PatentIn version 3.3  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 3763  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Homo sapiens  
 25 <400> SEQUENCE: 1  
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 28 gctgcacaat cagaagcagg cggaggagac ggcggccttc gaggagggtca tgaaggacct 120  
 30 gagcctgacg cgggccgcgc ggctccaggg ttcttgtaa agaaaacagg tagttaacct 180  
 32 atctcctgcc aacagcaagc gacccaatgg ctttgtggac aactcatttc ttgatataca 240  
 34 aagaattcgt gttggggaga atctctctgc aggacaagg ggctccaaa taaacaatgg 300  
 36 acaaagtcag attatgtcag ggaccttgcc tatgagccaa gacccctgc gaaagactaa 360  
 38 cactctgcca tccatacac attctcctgg caatggcctg tttaacatgg gcttaaagga 420  
 40 ggtaaagaag gagccaggag agactctgtc ttgcagtaag cacatggatg gccaaatgac 480  
 42 ccaagagaat attttcccta ataggtagcg agacgacct ggagaacaac tgatggatcc 540  
 44 tgagctgcag gaactgttca atgaactgac caacatatct gtgcctccca tgagtgcact 600  
 46 tgaactggag aacatgatca atgccaccat aaagcaggat gacccattta acattgactt 660  
 48 gggtcagcaa agccagagga gcacacctag gccctcctta cccatggaga aaatagtgat 720  
 50 caaaagtga taccaccgg gcttgactca gggccctca ggctctcctc agctgaggcc 780  
 52 cccatcagct ggccccgcct tctccatggc caactctgcc ctctccaact cgtctccaat 840  
 54 cccttcagtc cctcagagcc aggtctagcc tcagacaggc tccggagcaa gccgggcctt 900  
 56 gccaaagctg caggaagtat cccatgcccc gcagctcaaa cagatagctg ctaatcgtca 960  
 58 gcagcatgcc cggatgcagc agcaccagca gcagcaccag cctaccaact ggtcagcctt 1020  
 60 gccctcctct gctggacct caccaggtcc atttgggcag gagaaaatcc ccagcccttc 1080  
 62 ttttgggtcag cagacattca gccacacag ctcccccatg cctggggtag ctggcggcag 1140  
 64 cggccagtcg aaagtaatgg ctaactacat gtacaaggcc ggccctcag cccaggggtg 1200  
 66 gcacctagat gtcctcatgc agcaaaagcc tcaggatctc agtcgaagtt ttattaacaa 1260  
 68 cccgcaccca gccatggagc ccgctcaggg caacaccaag cctttgtttc attttaactc 1320  
 70 agatcaagcg aaccagcaga tgcttctgt tttgccttcc cagaacaagc cttctctcct 1380  
 72 acactacacc caacagcaac agcagcaaca gcagcagcag cagcagcagc agcagcagca 1440  
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 76 acaacagcaa cagcagcaga gctcaatttc agcccaacag cagcagcagc agcaacaaca 1560  
 78 gcagcagcag cagcaacaac aacagcaaca acagcagcag cagcagcagc aacaaccatc 1620

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80 ttctcagcct gcccaatctc taccaagcca gcctttgcta aggtcacctt tgccacttca 1680
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84 ctcccaacaa cagagacagg atcaaacactc tgtggtaggc cagaacacag gcccagtc 1800
86 aagtcctaac cctgctcaa atccaaacac tggaagtggc tacatgaact cccagcaatc 1860
88 actgttgaat cagcaattga tgggaaagaa gcagactcta cagaggcaga tcatggagca 1920
90 gaaacagcaa cttcttctcc agcagcagat gctggctgac gcggagaaaa ttgctccaca 1980
92 agatcagata aaccgacatt tgtcaaggcc acctccagat tataaagacc aaagaagaaa 2040
94 tgtgggcaat atgcaaccaa ctgctcagta ttctgggtggc tcatccacaa taagcttaaa 2100
96 ctctaaccag gctttggcaa acccagtttc aacacacacc attttaactc ccaattccag 2160
98 cctcctgtct acttctcagc ggacaagaat gccatcatta tctacagcag ttcagaatat 2220
100 ggggatgtat ggaaatctgc cttgtaatca acctaacaca tacagtgtca cttcaggaat 2280
102 gaatcaattg acccaacaga gaaacccaaa gcaattgtta gcaaatcaaa acaacctat 2340
104 gatgccacgg ccacctacct tagggccaag taataataac aatgtagcca cttttggagc 2400
106 tggatctgtt ggtaattcac aacaattgag accaaattta acccatagta tggcaagcat 2460
108 gccaccacag agaacatcaa acgtaatgat cacatccaac acaactgcac caaactgggc 2520
110 ctctcaagaa ggaacaagca aacagcaaga agccctgacg tctgcaggag tccgcttccc 2580
112 cacaggtaga cctgcagcct ataccccaaa tcagtcactg caacaggcag taggtagcca 2640
114 gcaattttcc cagagggcag tggtcctccc taaccagtta acaccagcag tgcaaatgag 2700
116 acccatgaac caaatgagcc aaacactaaa tgggcaaacc atgggtcccc tcaggggtct 2760
118 gaatctcaga ccaatcagc taagcacaca gattttgcct aatttgaatc agtcaggaac 2820
120 agggttgaat cagtcagga cgggcatcaa ccagccacca tccctgacgc ccagcaattt 2880
122 tccttcaccc aaccaaagtt ccagggtctt tcaaggaaact gaccacagca gtgacttagc 2940
124 ttttgacttc ctcagccaac aaaatgataa catgggcccct gccctaaaca gtgatgctga 3000
126 tttcattgat tctttattga agacagagcc tggtaatgat gactggatga aagacatcaa 3060
128 tcttgatgaa atcttgggga acaattccta aagaagaaag ggaagacaat ttacaaactc 3120
130 caagcactaa aaggcagtat attacagaaa ctctgtagag gctgaactgt tgatgttcag 3180
132 gtggactaca tgaagataac atgcttaaaa atggaaagca gaaagtaact gcagtgtatga 3240
134 acattttggc ccaaattcct gttttaaatc ttacacctga aagtaaaata ttgggatcac 3300
136 ttttcctgt ctaactcca ggatacagta tccaatttat ccaaacagaa ctgtggtgtc 3360
138 aatgtgtaat taattgtgta aaatagcctt cccaagtctt tttttccctg gaaaataaaa 3420
140 aaggtaatag aacttgtagt ttatttaaac cccatgtcat gaggaggtag tagttccaag 3480
142 caacaaactc cttaatttgc tctaatagat aggtatgggt taatctttcc attgtgtctt 3540
144 ttcatttaat tttcctgaag cttgcaggat agattgaaat gttatagggt tgtttggagt 3600
146 aaccaaacag tatgcaaatt aagaaaaagc cagagaacct agaaaacatc cagtggatta 3660
148 cagaatttct tccccatatt cactcctcac ttttacaatt tccccacaat cctctacttc 3720
150 agtgggatgc tgtgtctagt gattaaacaa aaatatagag ctg 3763

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153 &lt;210&gt; SEQ ID NO: 2

154 &lt;211&gt; LENGTH: 73

155 &lt;212&gt; TYPE: DNA

156 &lt;213&gt; ORGANISM: Unknown

158 &lt;220&gt; FEATURE:

159 &lt;223&gt; OTHER INFORMATION: RNAi clone

161 &lt;400&gt; SEQUENCE: 2

162 ttggcaggag atagggttaac tacctgttga agcttgagca ggtgggttaat ctatctcctg 60

164 ctaacagttt ttt 73

167 &lt;210&gt; SEQ ID NO: 3

168 &lt;211&gt; LENGTH: 71

169 &lt;212&gt; TYPE: DNA

170 &lt;213&gt; ORGANISM: Unknown

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172 <220> FEATURE:
173 <223> OTHER INFORMATION: RNAi clone
175 <400> SEQUENCE: 3
176 atgtgcagcg cgatcttctc gctgaatgaa gcttgattcg gcgagaaggt cgcgttgcac      60
177 gatcagtttt t                                                                71
181 <210> SEQ ID NO: 4
182 <211> LENGTH: 78
183 <212> TYPE: DNA
184 <213> ORGANISM: Unknown
186 <220> FEATURE:
187 <223> OTHER INFORMATION: RNAi clone - antisense
189 <400> SEQUENCE: 4
190 gatcaaaaaa ctgatcgtgc aacgcgacct tctgccgaat caagcttcat tcagcgagaa      60
191 gatcgcgctg cacaatcg                                                                78
195 <210> SEQ ID NO: 5
196 <211> LENGTH: 28
197 <212> TYPE: DNA
198 <213> ORGANISM: Unknown
200 <220> FEATURE:
201 <223> OTHER INFORMATION: fragment of Mect1-MAML2 sequence
203 <400> SEQUENCE: 5
204 ttggcaggag ataggttaac tacctggt                                                                28
207 <210> SEQ ID NO: 6
208 <211> LENGTH: 28
209 <212> TYPE: DNA
210 <213> ORGANISM: Unknown
212 <220> FEATURE:
213 <223> OTHER INFORMATION: fragment of Mect1-MAML2 sequence
215 <400> SEQUENCE: 6
216 attgtgcagc gcgatcttct cgctgaat                                                                28
219 <210> SEQ ID NO: 7
220 <211> LENGTH: 28
221 <212> TYPE: DNA
222 <213> ORGANISM: Unknown
224 <220> FEATURE:
225 <223> OTHER INFORMATION: fragment of Mect1-MAML2 sequence
227 <400> SEQUENCE: 7
228 attcagcgag aagatcgcg tgcacaac                                                                28
231 <210> SEQ ID NO: 8
232 <211> LENGTH: 19
233 <212> TYPE: RNA
234 <213> ORGANISM: Unknown
236 <220> FEATURE:
237 <223> OTHER INFORMATION: siRNA #1
239 <400> SEQUENCE: 8
240 ccuaucuccu gccaacagc                                                                19
243 <210> SEQ ID NO: 9
244 <211> LENGTH: 19
245 <212> TYPE: RNA

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246 <213> ORGANISM: Unknown
248 <220> FEATURE:
249 <223> OTHER INFORMATION: complement to siRNA #1
251 <400> SEQUENCE: 9
252 gcuguuggca ggagauagg                                     19
255 <210> SEQ ID NO: 10
256 <211> LENGTH: 19
257 <212> TYPE: RNA
258 <213> ORGANISM: Unknown
260 <220> FEATURE:
261 <223> OTHER INFORMATION: siRNA #2
263 <400> SEQUENCE: 10
264 cagguaguua accuauauc                                     19
267 <210> SEQ ID NO: 11
268 <211> LENGTH: 19
269 <212> TYPE: RNA
270 <213> ORGANISM: Unknown
272 <220> FEATURE:
273 <223> OTHER INFORMATION: complement to siRNA #2
275 <400> SEQUENCE: 11
276 gagauagguu aacuaccug                                     19
279 <210> SEQ ID NO: 12
280 <211> LENGTH: 1024
281 <212> TYPE: PRT
282 <213> ORGANISM: Homo sapiens
284 <400> SEQUENCE: 12
286 Met Ala Thr Ser Asn Asn Pro Arg Lys Phe Ser Glu Lys Ile Ala Leu
287 1          5          10          15
290 His Asn Gln Lys Gln Ala Glu Glu Thr Ala Ala Phe Glu Glu Val Met
291          20          25          30
294 Lys Asp Leu Ser Leu Thr Arg Ala Ala Arg Leu Gln Gly Ser Leu Lys
295          35          40          45
298 Arg Lys Gln Val Val Asn Leu Ser Pro Ala Asn Ser Lys Arg Pro Asn
299          50          55          60
302 Gly Phe Val Asp Asn Ser Phe Leu Asp Ile Lys Arg Ile Arg Val Gly
303 65          70          75          80
306 Glu Asn Leu Ser Ala Gly Gln Gly Gly Leu Gln Ile Asn Asn Gly Gln
307          85          90          95
310 Ser Gln Ile Met Ser Gly Thr Leu Pro Met Ser Gln Ala Pro Leu Arg
311          100         105         110
314 Lys Thr Asn Thr Leu Pro Ser His Thr His Ser Pro Gly Asn Gly Leu
315          115         120         125
318 Phe Asn Met Gly Leu Lys Glu Val Lys Lys Glu Pro Gly Glu Thr Leu
319          130         135         140
322 Ser Cys Ser Lys His Met Asp Gly Gln Met Thr Gln Glu Asn Ile Phe
323 145         150         155         160
326 Pro Asn Arg Tyr Gly Asp Asp Pro Gly Glu Gln Leu Met Asp Pro Glu
327          165         170         175
330 Leu Gln Glu Leu Phe Asn Glu Leu Thr Asn Ile Ser Val Pro Pro Met

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331          180          185          190
334 Ser Asp Leu Glu Leu Glu Asn Met Ile Asn Ala Thr Ile Lys Gln Asp
335          195          200          205
338 Asp Pro Phe Asn Ile Asp Leu Gly Gln Gln Ser Gln Arg Ser Thr Pro
339          210          215          220
342 Arg Pro Ser Leu Pro Met Glu Lys Ile Val Ile Lys Ser Glu Tyr Ser
343 225          230          235          240
346 Pro Gly Leu Thr Gln Gly Pro Ser Gly Ser Pro Gln Leu Arg Pro Pro
347          245          250          255
350 Ser Ala Gly Pro Ala Phe Ser Met Ala Asn Ser Ala Leu Ser Thr Ser
351          260          265          270
354 Ser Pro Ile Pro Ser Val Pro Gln Ser Gln Ala Gln Pro Gln Thr Gly
355          275          280          285
358 Ser Gly Ala Ser Arg Ala Leu Pro Ser Trp Gln Glu Val Ser His Ala
359          290          295          300
362 Gln Gln Leu Lys Gln Ile Ala Ala Asn Arg Gln Gln His Ala Arg Met
363 305          310          315          320
366 Gln Gln His Gln Gln Gln His Gln Pro Thr Asn Trp Ser Ala Leu Pro
367          325          330          335
370 Ser Ser Ala Gly Pro Ser Pro Gly Pro Phe Gly Gln Glu Lys Ile Pro
371          340          345          350
374 Ser Pro Ser Phe Gly Gln Gln Thr Phe Ser Pro Gln Ser Ser Pro Met
375          355          360          365
378 Pro Gly Val Ala Gly Gly Ser Gly Gln Ser Lys Val Met Ala Asn Tyr
379          370          375          380
382 Met Tyr Lys Ala Gly Pro Ser Ala Gln Gly Gly His Leu Asp Val Leu
383 385          390          395          400
386 Met Gln Gln Lys Pro Gln Asp Leu Ser Arg Ser Phe Ile Asn Asn Pro
387          405          410          415
390 His Pro Ala Met Glu Pro Arg Gln Gly Asn Thr Lys Pro Leu Phe His
391          420          425          430
394 Phe Asn Ser Asp Gln Ala Asn Gln Gln Met Pro Ser Val Leu Pro Ser
395          435          440          445
398 Gln Asn Lys Pro Ser Leu Leu His Tyr Thr Gln Gln Gln Gln Gln Gln
399          450          455          460
402 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
403 465          470          475          480
406 Gln Gln Gln Gln Gln Gln Gln Gln Gln Ser Ile Ser Ala Gln Gln
407          485          490          495
410 Gln Gln Gln Gln Gln Ser Ser Ile Ser Ala Gln Gln Gln Gln Gln Gln
411          500          505          510
414 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
415          515          520          525
418 Gln Gln Gln Gln Gln Pro Ser Ser Gln Pro Ala Gln Ser Leu Pro Ser
419          530          535          540
422 Gln Pro Leu Leu Arg Ser Pro Leu Pro Leu Gln Gln Lys Leu Leu Leu
423 545          550          555          560
426 Gln Gln Met Gln Asn Gln Pro Ile Ala Gly Met Gly Tyr Gln Val Ser
427          565          570          575

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